

WE CLAIM:

1. A composition comprising a protein in crystalline form wherein the protein has at least 90% identity with residues 2-384 of SEQ. ID No. 1.
2. A composition according to claim 1 wherein the protein has at least 95% identity with residues 2-384 of SEQ. ID No. 1.
3. A composition according to claim 1 wherein the protein comprises consecutively of residues 2-384 of SEQ. ID No. 1.
4. A composition according to claim 1 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.
5. A composition according to claim 1 wherein the protein crystal has a crystal lattice in a $P2_12_12_1$ space group.
6. A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, $\pm 5\%$, of $a=68.7$ $b=79.6$ $c=150.2$, $\alpha=\beta=\gamma=90$.
7. A method for forming a crystal of a protein comprising:
forming a crystallization volume comprising: a precipitant solution and a protein wherein at least a portion of the protein has at least 90% identity with residues 2-384 of SEQ. ID No. 1; and
storing the crystallization volume under conditions suitable for crystal formation of the protein.
8. A method according to claim 7 wherein the protein has at least 95% identity with residues 2-384 of SEQ. ID No. 1.
9. A method according to claim 7 wherein the protein comprises consecutively of residues 2-384 of SEQ. ID No. 1.
10. A method according to claim 7 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

11. A method according to claim 7 wherein the protein crystal has a crystal lattice in a $P2_12_12_1$ space group.
12. A method according to claim 7 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of $a=68.7$ $b=79.6$ $c=150.2$, $\alpha=\beta=\gamma=90$.
13. A method according to claim 7, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.
14. A composition comprising an isolated protein consisting of residues 2-384 of SEQ. ID No. 1.
15. A composition according to claim 14 where the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.
16. A composition comprising an isolated protein consisting of SEQ. ID No. 1.
17. A method of identifying an entity that associates with a protein comprising:
taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ. ID No. 1; and
performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.
18. A method according to claim 17 wherein the protein has at least 95% identity with SEQ. ID No. 1.
19. A method according to claim 17 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of $a=68.7$ $b=79.6$ $c=150.2$, $\alpha=\beta=\gamma=90$.
20. A method according to claim 17, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

21. A method according to claim 17, the method further comprising measuring an activity of the protein when contacted with the one or more entities.
22. A method according to claim 17, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present.
23. A method according to claim 17, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.